## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compug Compugen Ltd.

OM nucleic nucleic search, using sw model

Run on: July 1, 2003, 14:30:42; Search time 367 Seconds (without alignments) 9314.805 Million cell updates/sec

Title: Perfect score: US-10-010-742-305 1518 1 atggagccctcctggcttca.....ttgcaaaaaagtttgctaa 1518

Scoring table: IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

. 2185239 seqs, 1125999159 residues

Searched:

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database N\_Geneseq\_101002:\* /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:\* /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:\* SIDS2/gcgdata,

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Query Query Match Length DB ID  100.0 2015 24 AAD24015 99.9 2020 24 ABK33550 67.8 1586 22 AAD09946 44.2 2343 22 AAS21297 44.3 2381 24 ABK63921 44.2 2416 22 AAD09941 43.4 2327 24 ABK52898	
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## ALIGNMENTS

RESULT 1 AAD24015

AAD24015 standard; cDNA; 2015 BP

AAD24015;

26-MAR-2002 (first entry)

Human drug metabolising enzyme (DME)-10 cDNA.

Human; drug metabolising enzyme; DME-10; autoimmune; inflammatory; cell proliferative; developmental; endocrine; eye; metabolic; AIDS; gastrointestinal disorder; liver disorder; cancer; arteriosclerosis; adult respiratory distress syndrome; anaemia; epilepsy; hypothyroidism; hypothalamus; pituitary; diabetes; hypogonadism; conjunctivitis; glaucoma; cystic fibrosis; hypercholesterolaemia; gastritis; peptic ulcer; hepatitis; gene therapy; ss.

Homo sapiens.

Location/Qualifiers /\*tag-

mat\_peptide sig\_peptide /\*tag- b 210..1631 /product= 117..209 \*Drug metabolising enzyme-10"

/product= "Mature drug metabolising enzyme-10"

WO200190334-A2

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2000WO-US33873
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Baker KP, De Grimaldi JC, WPI; 2002-172001/22. Desnoyers Gurney Ąŗ, Gerritsen ME, Goddard Smith V, Stephan JF, Goddard A, Godowski PJ; phan JF, Watanabe CK, Wood ž

One hundred and twenty two nucleic acids encoding PRO polypeptides, useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour

Claim 2; Figure 29; 359pp; English.

The invention relates to one hundred and twenty two nucleic acids cancoding PRO polypeptides. The sequences of the 122 PRO polypucleotides cancode human secreted proteins. The PRO nucleic acids, polypucleotides, agonists and antagonists are useful for treating a PRO related disorder. The PRO polypeptides are useful for diagnosing tumours, especially lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the proliferation of, or gene expression, in pericyte cells, for stimulating the proliferation or differentiation of chondrocyte cells, for stimulating the proliferation of normal human blood, for stimulating the release of the unour necrosis factor-alpha from human blood, for stimulating or inhibiting the proliferation of normal human dermal control of the proliferation of normal human dermal inbobast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular bloody, including use as hybridisation probes, and in chromosome and gene mapping. ABK33536-ABK33657 represent human property.

Sequence 2020 BP; 573 A; 489 C; 409 G; 549 T; 0 other;

Query Match
Best Local Similarity
Matches 1517; Conserv Conservative 99.98; Pred. No. 0; 0; Mismatches DB 24; Length 1: Indels 2020; **0** Gaps 0

ŊΥ	_	ATGGAGCCCTCCTGGCTTCAGGAACTCATGGCTCACCCCTTCTTGCTGCTGATCCTCCTC 60	
Ъ	117	AIGGAGCCCICCIGCCITCAGGAACICAIGGCICACCCCIICTIGCIGCIGAICCCICCIC 176	σ
¥Ω	61	TGCATGTCTCTGCTGCTGTTTCAGGTAATCAGGTTGTACCAGAGGAGGAGGAGGATGATC 120	0
9	177	TGCATGTCTCTGCTGCTGTTTCAGGTAATCAGGTTGTACCAGAGGAGGAGATGGATG	σ
Οy	121	AGAGCCCTGCACCTGTTTCCTGCACCCCCTGCCCACTGGTTCTATGGCCACAAGGAGTTT 180	0
9	237	AGAGCCCTGCACCTGTTTCCTGCACCCCCTGCCCACTGGTTCTATGGCCACAAGGAGTTT 296	0
Δy	181	TACCCAGTAAAGGAGTTTGAGGTGTATCATAAGCTGATGGAAAAAATACCCATGTGCTGTT 240	0
9	297	TACCGAGTAAAGGAGTTTGAGGTGTATCATAAGCTGATGGAAAAATACCCATGTGCTGTT 356	σ
Σy	241	CCCTTGTGGGTTGGACCCCTTTACGATGTTCTTCAGTGTCCATGACCCAGACTATGCCAAG 300	0
9	357	CCCTTGTGGGTTGGACCCTTTACGATGTTCTTCAGTGTCCATGACCCAGACTATGCCAAG 416	σ
ŊΥ	301	ATTCTCCTGAAAAGACAAGATCCCAAAAAGTGCTGTTAGCCACAAAAATCCTTGAATCCTGG 360	0
8	417	ATTCTCCTGAAAAGACAAGATCCCAAAAGTGCTGTTAGCCACAAAATCCTTGAATCCTGG 476	σ
ŊΥ	361	GTTGGTCGAGGACTTGTGACCCTGGATGGTTCTAAATGGAAAAAGCACCGCCAGATTGTG 420	0
ᅜ	477	GTTGGTCGAGGACTTGTGACCCTGGATGGTTCTAAATGGAAAAAGCACCGCCAGATTGTG 536	O.
Ϋ́	421	AAACCTGGCTTCAACATCAGCATTCTGAAAATATTCATCACCATGATGTCTGAGAGTGTT 480	0
8	537	AAACCTGGCTTCAACATCAGCATTCTGAAAATATTCATCACCATGATGTCTGAGAGTGTT 596	σı
<b>γ</b> .	481	CGGATGATGCTGAACAAATGGGAAGGAACGCATTGCCCAAAAACTCACGTCTGGAAGCTCTTT 540	0
퓻	597	CGGATGATGCTGAACAAATGGGAGGAACACATTGCCCAAAAACTCACGTCTGGAGCTCTTT 656	on

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